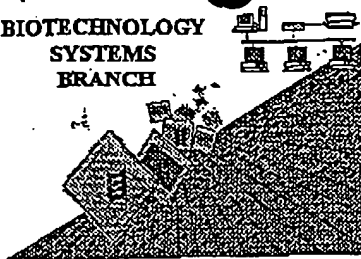


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



PK

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,918  
Source: Pt/09  
Date Processed by STIC: 9/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/673,918

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1. Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
3. Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5. Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6. PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused file <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7. Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8. Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
9. Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10. Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11. Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12. PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13. Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

PCT09

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/673,918

DATE: 09/05/2001  
 TIME: 14:37:47

Input Set : A:\16430seq.txt  
 Output Set: N:\CRF3\09052001\I673918.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Xia, Zhi-Qiang  
 4 Costa, Michael A  
 5 Davin, Laurence B  
 6 Lewis, Norman G  
 8 <120> TITLE OF INVENTION: Recombinant Secoisolariciresinol Dehydrogenase, and  
 9 Methods of Use  
 11 <130> FILE REFERENCE: WSUR116430  
 13 <140> CURRENT APPLICATION NUMBER: 09/673,918  
 14 <141> CURRENT FILING DATE: 2001-05-30  
 16 <150> PRIOR APPLICATION NUMBER: PCT/US99/08975  
 17 <151> PRIOR FILING DATE: 1999-04-23  
 19 <150> PRIOR APPLICATION NUMBER: 60/082,977  
 20 <151> PRIOR FILING DATE: 1998-04-24  
 22 <160> NUMBER OF SEQ ID NOS: 25  
 24 <170> SOFTWARE: PatentIn Ver. 2.0

# ERRORED SEQUENCES

395 <210> SEQ ID NO: 6  
 396 <211> LENGTH: 273  
 397 <212> TYPE: PRT  
 398 <213> ORGANISM: Forsythia x intermedia  
 400 <400> SEQUENCE: 6  
 401 Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala  
 402 1 5 10 15  
 404 Leu Ile Thr Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu  
 405 20 25 30  
 407 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu  
 408 35 40 45  
 410 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr  
 411 50 55 60  
 413 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 414 65 70 75 80  
 416 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala  
 417 85 90 95  
 419 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala  
 420 100 105 110  
 --> 422 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe  
 423 115 120 125  
 425 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile  
 426 130 135 140  
 428 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His  
 429 145 150 155 160  
 431 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu  
 432 165 170 175  
 434 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro

file://C:\CrF3\Outhold\Vsrl673918.htm

9/5/01

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/673,918

DATE: 09/05/2001  
 TIME: 14:37:47

Input Set : A:\16430seq.txt  
 Output Set: N:\CRF3\09052001\I673918.raw

```

435          180          185          190
437 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
438          195          200          205
440 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
441          210          215          220
443 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
444 225          230          235          240
446 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
447          245          250          255
449 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
450          260          265          270
452 Ser
  
```

*psl* Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

file://C:\CrF3\Outhold\VsrI673918.htm

9/5/01

VERIFICATION SUMMARY  
 PATENT APPLICATION: US/09/673,918

DATE: 09/05/2001  
 TIME: 14:37:48

Input Set : A:\16430seq.txt  
 Output Set: N:\CRF3\09052001\I673918.raw

:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 :351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 :351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 :352 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 :352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 :422 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
 :758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
 :761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
 :804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
 :823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 :842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 :879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

*Xaa represents any amino acid.*

*<223> c)NA molecule encoding seconolavikiresinol  
 dehydrogenase wherein Xaa ~~at position~~ represents any amino  
 acid.*

file://C:\Crf3\Outhold\Vsrl673918.htm

9/5/01